

Resource Summary Report

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Blast2GO

RRID:SCR_005828

Type: Tool

Proper Citation

Blast2GO (RRID:SCR_005828)

Resource Information

URL: <http://www.blast2go.com/b2ghome>

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Description: An ALL in ONE tool for functional annotation of (novel) sequences and the analysis of annotation data. Blast2GO (B2G) joins in one universal application similarity search based GO annotation and functional analysis. B2G offers the possibility of direct statistical analysis on gene function information and visualization of relevant functional features on a highlighted GO direct acyclic graph (DAG). Furthermore B2G includes various statistics charts summarizing the results obtained at BLASTing, GO-mapping, annotation and enrichment analysis (Fisher's Exact Test). All analysis process steps are configurable and data import and export are supported at any stage. The application also accepts pre-existing BLAST or annotation files and takes them to subsequent steps. The tool offers a very suitable platform for high throughput functional genomics research in non-model species. B2G is a species-independent, intuitive and interactive desktop application which allows monitoring and comprehending the whole annotation and analysis process supported by additional features like GO Slim integration, evidence code (EC) consideration, a Batch-Mode or GO-Multilevel-Pies. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: B2G

Synonyms: Blast2GO (B2G)

Resource Type: software resource, software application

Defining Citation: [PMID:16081474](#)

Keywords: annotation, visualization, analysis, functional genomics, editor, statistical analysis, slimmer-type tool, ontology or annotation editor, functional analysis, direct acyclic graph, analysis, high throughput, functional genomics

Funding: MCyT GEN 2001 - 4885-C05-03;
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Availability: Free for academic use

Resource Name: Blast2GO

Resource ID: SCR_005828

Alternate IDs: OMICS_01475, nlx_149335

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260818T043240+0000

Ratings and Alerts

No rating or validation information has been found for Blast2GO.

No alerts have been found for Blast2GO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8620 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. BMC biology, 24(1).

Dombaxe CP, et al. (2026) Proteomic Signatures of Regeneration: Uncovering Extracellular Matrix-Associated Cues in Goldfish Spinal Cord Repair. The Journal of comparative neurology, 534(5), e70170.

Li Y, et al. (2026) Enhanced STEAP4 Ubiquitination in Obesity: Insights From Combined Proteome and Ubiquitylome Analysis of Visceral Adipose Tissue. Molecular & cellular proteomics : MCP, 25(1), 101474.

Wu K, et al. (2026) Deciphering the role of ThHSF1 in the differential expression regulation of laccase isozymes in the white-rot fungus Trametes hirsuta. Microbiology spectrum, 14(1), e0100425.

Ma Y, et al. (2026) Transcriptomic differences in immune- and stress-related pathways associated with artificial rearing in the endangered hog deer (Axis porcinus). BMC genomics, 27(1), 196.

Wei X, et al. (2026) Genetic Control of Tissue Remodeling by a Non-Coding SNP in ITGA8 Explains Carotenoid-Based Color Polymorphism in Marine Mollusks. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(27), e20527.

Barba de la Rosa AP, et al. (2026) Transcriptome and metabolite profiles reveal differential molecular responses of wild and cultivated amaranth species to water deficit and salt stress. *Planta*, 263(3), 59.

Tahiri G, et al. (2026) Coordinated gene family evolution shapes the genome of dimorphic *Mucorales*. *Nature communications*, 17(1).

Chen P, et al. (2026) Upregulation of LTF promotes left-sided colorectal cancer development via activating PI3K/AKT pathway. *Cell adhesion & migration*, 20(1), 2613628.

Peng X, et al. (2026) Integrated Phosphoproteomics Identifies TGF β -Dependent Phosphorylation Events Linking Kinase Signaling to Autophagy in Palatogenesis. *Proteomes*, 14(1).

Cury NF, et al. (2026) Aluminum-induced proteomic responses in *Qualea dichotoma* (Mart.) warm: a dataset descriptive analysis. *Scientific reports*, 16(1).

Byrne AQ, et al. (2026) Genomic Correlates of Disease Recovery in Natural Populations of the Sierra Nevada Yellow-Legged Frog (*Rana sierrae*). *Molecular ecology*, 35(8), e70348.

Bessho-Uehara M, et al. (2026) Absence of the luciferase gene in the genome of the kleptoprotein bioluminescent fish *Parapriacanthus ransonneti*. *Scientific reports*, 16(1).

Gul A, et al. (2026) Rosmarinic acid alleviates bleomycin-induced pulmonary fibrosis in mice by activating the Rap1 pathway. *Scientific reports*, 16(1).

Bai H, et al. (2026) Characterization of the gut phageome and functional genes carried by phages in laying hens with fatty liver hemorrhagic syndrome. *Microbiome*, 14(1).

Chen YZ, et al. (2026) Whole-Genome Sequencing of Pathogenic *Nigrospora musae* ST1 Causing Leaf Spot Disease in *Idesia polycarpa*. *Journal of fungi* (Basel, Switzerland), 12(3).

de Oliveira GL, et al. (2026) Genome-wide association study in a diverse grapevine collection provides insights into the genetic basis of berry size and cluster architecture traits. *PloS one*, 21(3), e0343491.

Pal D, et al. (2026) Integrative transcriptome and genome resequencing reveals conserved flowering regulators and allelic variants in early- and late-flowering linseed (*Linum usitatissimum* L.) accessions. *Scientific reports*, 16(1).

Tepa A, et al. (2026) Transcriptomic signatures of high-intensity pyrethroid resistance in *Anopheles gambiae* from a Cameroonian agricultural hotspot. *BMC genomics*, 27(1).

Weng K, et al. (2026) Comparative phosphoproteomic analysis reveals regulatory mechanisms underlying muscle fiber density in goslings. *Poultry science*, 105(6), 106725.